Amendments to the Specification:

A. Please replace the 4th full paragraph on p. 7, at lines 18 to 22, with the following amended paragraph:

ΦSchematic representation of gene promoters created by using Celera web-based genomic database to obtain 5' regulatory region, followed by theoretical analysis using TESS promoter analysis software ~~(http://www.cbil.upenn.edu/tess/)~~ and the TRANSFAC transcription factor database. Relevant consensus sequence matches are in accordance with published literature.

B. Please replace the last full paragraph on page 31 with the following amended paragraph:

B cell isolation, target preparation, and hybridization using Affymetrix Mu6500 microarrays were performed as described previously (Dadgostar, H., Zarnegar, B., Hoffman, A., Qin, X.-F., Truong, U., Rao, G., Baltimore, D., and Cheng, G. (2002), Proc. Natl. Acad. Sci. USA 99, 1497-1502). Differential expression data was analyzed by Affymetrix Microarray Suite 4.0 software. Average difference change values were then normalized and the genes were clustered by the uncentered correlation average linkage hierarchical clustering algorithm using Cluster. Data was then visualized as a dendogram using Treeview software ~~(www.rana.lbl.gov/EisenSoftware.htm)~~.

C. Please replace the last full paragraph on page 37 with the following amended paragraph:

A summary of five TLR3/TLR4-specific primary response genes--IP10, RANTES, IFNβ, ISG15 and IFIT1--is shown in FIG. 2D. These genes have been studied by other groups primarily in the context of viral infection and interferon stimulation (IP-10, (Cole, A. M., Ganz, T., Liese, A. M., Burdick, M. D., Liu, L., and Strieter, R. M. (2001), J. Immunol. 167, 623-627; Ohmori, Y., and Hamilton, T. A. (1993), J. Biol. Chem. 268, 6677-6688; Proost, P., Schutyser, E., Menten, P., Struyf, S., Wuyts, A., Opdenakker, G., Detheux, M., Parmentier,

M., Durinx, C., Lambeir, A. M., et al. (2001), Blood 98, 3554-3561); RANTES, (Lin, R., Heylbroeck, C., Genin, P., Pitha, P. M., and Hiscott, J. (1999), Mol. Cell. Biol. 19, 959-966; Luther, S. A., and Cyster, J. G. (2001), Nat. Immunol. 2, 102-107; Wagner, L., Yang, O. O., Garcia-Zepeds, E. A., Ge, Y., Kalams, S. A., Walker, B. D., Pastemack, M. S., and Luster, A. D. (1998), Nature 391, 908-911); IFN.beta., (Taniguchi, T., and Takaoka, A. (2002), Curr. Opin. Immunol. 14, 111-116); ISG15, (D'Cunha, J., Knight, E., Haas, A. L., Truitt, R. L., and Borden, E. C. (1996), Proc. Natl. Acad. Sci. USA 93, 211-215); IFIT1, (Guo, J., and Sen, G. C. (2000), J. Virol. 74, 1892-1899; Smith, J. B., and Herschman, H. R. (1996), Arch. Biochem. Biophys. 330, 290-300). To identify common elements that might mediate TLR3/TLR4-specific gene induction, we analyzed the gene promoters using the 5' one kilobase sequence obtained from Celera proprietary murine genomic databases and TESS promoter analysis software ~~(http://www.cbil.upenn.edu/tess/)~~. The regulatory regions of all five genes showed high probability matches for ISRE and κB consensus sequences (Max. lg=>28.0) within a few hundred base pairs of the transcriptional start site (FIG. 2D). This indicated that these genes may be co-regulated by common activators which bind at these sites.